

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: April 4, 2006, 18:17:09 ; Search time 138.5 Seconds
 (without alignments)
 545.655 Million cell updates/sec

Title: US-10-825-068-2
 Perfect score: 907
 Sequence: 1 CYLSRKMLDARENKLLDR.....TVSTTLQKRLTKMGGDLNSP 172

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : A_Geneseq_21:*
 1: geneseqp1980s:*
 2: geneseqp1990s:*
 3: geneseqp2000s:*
 4: geneseqp2001s:*
 5: geneseqp2002s:*
 6: geneseqp2003as:*
 7: geneseqp2003bs:*
 8: geneseqp2004s:*
 9: geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	907	100.0	172	2	AAR54768	Aar54768 Sheep int
2	907	100.0	172	2	AAR99397	Aar99397 Ovine tau
3	907	100.0	172	2	AAW31698	Aaw31698 Mature ov
4	907	100.0	172	2	AAW44110	Aaw44110 Mature ov
5	907	100.0	172	5	ABB07588	Abb07588 Ovine int
6	907	100.0	172	7	ADI17857	Adi17857 Mature ov
7	907	100.0	172	8	ADM79177	Adm79177 Mature ov
8	907	100.0	172	8	ADS13613	Ads13613 Sheep int

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OM protein - protein search, using sw model

Run on: April 4, 2006, 18:27:09 ; Search time 34 Seconds
 (without alignments)
 418.242 Million cell updates/sec

Title: US-10-825-068-2
 Perfect score: 907
 Sequence: 1 CYLSRKMLLDARENKLLDR.....TVSTTLQKRLTKMGGDLNSP 172

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : Issued_Patents_AA:*
 1: /cgn2_6/ptodata/1/iaa/5_COMB.pep:*
 2: /cgn2_6/ptodata/1/iaa/6_COMB.pep:*
 3: /cgn2_6/ptodata/1/iaa/H_COMB.pep:*
 4: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
 5: /cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
 6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		Length	DB	ID	Description
		Match	Length				
1	907	100.0	172	1	US-08-438-753B-2	Sequence 2, Appli	
2	907	100.0	172	1	US-08-443-883A-2	Sequence 2, Appli	
3	907	100.0	172	1	US-08-631-328-2	Sequence 2, Appli	
4	907	100.0	172	1	US-08-455-524B-2	Sequence 2, Appli	
5	907	100.0	172	1	US-08-455-021B-2	Sequence 2, Appli	
6	907	100.0	172	2	US-09-045-467-2	Sequence 2, Appli	
7	907	100.0	172	2	US-08-954-395A-18	Sequence 18, Appl	
8	907	100.0	172	2	US-08-616-904-2	Sequence 2, Appli	
9	907	100.0	172	2	US-10-029-890-2	Sequence 2, Appli	
10	900	99.2	172	2	US-09-599-413-2	Sequence 2, Appli	
11	898	99.0	172	2	US-09-599-413-7	Sequence 7, Appli	

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OM protein - protein search, using sw model

Run on: April 4, 2006, 18:28:04 ; Search time 115 Seconds
 (without alignments)
 624.927 Million cell updates/sec

Title: US-10-825-068-2
 Perfect score: 907
 Sequence: 1 CYLSRKMLLDARENKLLDR.....TVSTTLQKRLTKMGDDLNSP 172

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : Published_Applications_AA_Main:*
 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
 2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
 3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
 4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
 5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
 6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	907	100.0	172	3	US-09-746-919-2	Sequence 2, Appli
2	907	100.0	172	3	US-09-910-406C-2	Sequence 2, Appli
3	907	100.0	172	4	US-10-029-890-2	Sequence 2, Appli
4	907	100.0	172	4	US-10-346-269-2	Sequence 2, Appli
5	907	100.0	172	4	US-10-346-269-3	Sequence 3, Appli
6	907	100.0	172	4	US-10-694-247-2	Sequence 2, Appli
7	907	100.0	172	4	US-10-683-214-1	Sequence 1, Appli
8	907	100.0	172	4	US-10-794-495-2	Sequence 2, Appli
9	907	100.0	172	4	US-10-719-472-2	Sequence 2, Appli
10	907	100.0	172	5	US-10-825-068-2	Sequence 2, Appli
11	907	100.0	172	5	US-10-884-741-2	Sequence 2, Appli

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OM protein - protein search, using sw model

Run on: April 4, 2006, 18:29:20 ; Search time 15.5 Seconds
(without alignments)
337.807 Million cell updates/sec

Title: US-10-825-068-2
Perfect score: 907
Sequence: 1 CYLSRKMLLDARENKLLDR.....TVSTTLQKRLTKMGGDLNSP 172

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 180808 seqs, 30441898 residues

Total number of hits satisfying chosen parameters: 180808

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA_New:*
1: /SIDS5/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
2: /SIDS5/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
3: /SIDS5/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
4: /SIDS5/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
5: /SIDS5/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
6: /SIDS5/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
7: /SIDS5/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
8: /SIDS5/ptodata/2/pubpaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		Length	DB	ID	Description
		Match	Length				
1	907	100.0	172	7	US-11-177-010-2	Sequence 2, Appli	
2	907	100.0	172	7	US-11-112-369-1	Sequence 1, Appli	
3	899	99.1	172	7	US-11-177-010-4	Sequence 4, Appli	
4	899	99.1	172	7	US-11-112-369-2	Sequence 2, Appli	
5	473	52.1	172	6	US-10-519-390-11	Sequence 11, Appl	
6	473	52.1	194	6	US-10-936-447-20	Sequence 20, Appl	
7	473	52.1	757	6	US-10-936-447-8	Sequence 8, Appli	
8	440	48.5	166	7	US-11-132-722-49	Sequence 49, Appl	
9	440	48.5	166	7	US-11-176-830-187	Sequence 187, App	

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OM protein - protein search, using sw model

Run on: April 4, 2006, 18:22:20 ; Search time 24.5 Seconds
 (without alignments)
 675.481 Million cell updates/sec

Title: US-10-825-068-2
 Perfect score: 907
 Sequence: 1 CYLSRKMLDARENKLLDR.....TVSTTLQKRLTKMGGDLNSP 172

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : PIR_80:*
 1: pir1:*
 2: pir2:*
 3: pir3:*
 4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	897	98.9	195	2	JS0204	trophoblast interf
2	880	97.0	195	2	I47068	trophoblast protei
3	868	95.7	195	2	I47066	trophoblast protei
4	865	95.4	195	2	I47069	trophoblast protei
5	847	93.4	172	2	A61578	trophoblast protei
6	846	93.3	195	2	I46272	trophoblast interf
7	842	92.8	195	2	A61455	trophoblast protei
8	806	88.9	195	2	I47067	trophoblast protei
9	778	85.8	195	2	I47097	trophoblast protei
10	745	82.1	184	2	I47098	trophoblast protei
11	724	79.8	195	2	A39505	trophoblast interf
12	723	79.7	195	2	S23751	trophoblast interf
13	720	79.4	195	2	B39505	trophoblast protei

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OM protein - protein search, using sw model

Run on: April 4, 2006, 18:17:34 ; Search time 145.5 Seconds
 (without alignments)
 834.027 Million cell updates/sec

Title: US-10-825-068-2
 Perfect score: 907
 Sequence: 1 CYLSRKMLLDARENKLLDR.....TVSTTLQKRLTKMGDDLNSP 172

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : UniProt_05.80:*
 1: uniprot_sprot:*
 2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	907	100.0	195	1 IFNT1_SHEEP	P56828 ovis aries
2	900	99.2	195	1 IFNT2_SHEEP	P56829 ovis aries
3	888	97.9	172	1 IFNT3_SHEEP	P56832 ovis aries
4	881	97.1	195	1 IFNT4_SHEEP	Q28594 ovis aries
5	880	97.0	195	1 IFNT7_SHEEP	Q08071 ovis aries
6	877	96.7	195	1 IFNT5_SHEEP	Q28595 ovis aries
7	868	95.7	195	1 IFNT9_SHEEP	Q08070 ovis aries
8	865	95.4	195	1 IFNT8_SHEEP	Q08072 ovis aries
9	846	93.3	195	1 IFNT_CAPHI	P28171 capra hircu
10	842	92.8	195	1 IFNT6_SHEEP	Q29429 ovis aries
11	830	91.5	195	2 Q6UZ49_CAPHI	Q6uz49 capra hircu
12	830	91.5	195	2 Q6UZ50_CAPHI	Q6uz50 capra hircu
13	816	90.0	172	2 Q6RFZ8_SHEEP	Q6rfz8 ovis aries
14	806	88.9	195	1 IFNTA_SHEEP	Q08053 ovis aries
15	804	88.6	195	2 Q6UZ47_CAPHI	Q6uz47 capra hircu

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OM protein - protein search, using sw model

Run on: April 4, 2006, 18:17:09 ; Search time 138.5 Seconds
(without alignments)
545.655 Million cell updates/sec

Title: US-10-825-068-3
Perfect score: 907
Sequence: 1 CYLSERLMLDARENKLLDR.....TVSTTLQKRLTKMGDDLNSP 172

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_21:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	907	100.0	172	5	ABB07589	Abb07589 Recombina
2	907	100.0	172	8	ADM79178	Adm79178 Mature ov
3	907	100.0	172	8	ADS13614	Ads13614 Recombina
4	907	100.0	172	9	AEA18013	Aea18013 Recombina
5	907	100.0	172	9	AEA39574	Aea39574 Recombina
6	901	99.3	195	2	AAR24941	Aar24941 Sequence
7	901	99.3	195	2	AAR24945	Aar24945 Sequence
8	899	99.1	172	2	AAR54768	Aar54768 Sheep int

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OM protein - protein search, using sw model

Run on: April 4, 2006, 18:27:09 ; Search time 34 Seconds
(without alignments)
418.242 Million cell updates/sec

Title: US-10-825-068-3
Perfect score: 907
Sequence: 1 CYLSERLMLDARENLKLLDR.....TVSTTLQKRLTKMGDDLNSP 172

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/1/iaa/5_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/6_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/H_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	899	99.1	172	1	US-08-438-753B-2	Sequence 2, Appli
2	899	99.1	172	1	US-08-443-883A-2	Sequence 2, Appli
3	899	99.1	172	1	US-08-631-328-2	Sequence 2, Appli
4	899	99.1	172	1	US-08-455-524B-2	Sequence 2, Appli
5	899	99.1	172	1	US-08-455-021B-2	Sequence 2, Appli
6	899	99.1	172	2	US-09-045-467-2	Sequence 2, Appli
7	899	99.1	172	2	US-08-954-395A-18	Sequence 18, Appli
8	899	99.1	172	2	US-08-616-904-2	Sequence 2, Appli
9	899	99.1	172	2	US-10-029-890-2	Sequence 2, Appli
10	894	98.6	172	2	US-09-599-413-18	Sequence 18, Appli
11	892	98.3	172	2	US-09-599-413-2	Sequence 2, Appli

OM protein - protein search, using sw model

Run on: April 4, 2006, 18:28:04 ; Search time 115 Seconds
 (without alignments)
 624.927 Million cell updates/sec

Title: US-10-825-068-3
 Perfect score: 907
 Sequence: 1 CYLSERLMLDARENLKLLDR.....TVSTTLQKRLTKMGDDLNSP 172

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : Published_Applications_AA_Main:*
 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
 2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
 3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
 4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
 5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
 6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep:*

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 score greater than or equal to the score of the result being printed,
 and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	907	100.0	172	3	US-09-910-406C-4	Sequence 4, Appli
2	907	100.0	172	4	US-10-683-214-2	Sequence 2, Appli
3	907	100.0	172	4	US-10-719-472-3	Sequence 3, Appli
4	907	100.0	172	5	US-10-825-068-3	Sequence 3, Appli
5	907	100.0	172	5	US-10-884-741-3	Sequence 3, Appli
6	907	100.0	172	5	US-10-825-382-3	Sequence 3, Appli
7	907	100.0	172	5	US-10-825-457-3	Sequence 3, Appli
8	907	100.0	172	5	US-10-824-710-3	Sequence 3, Appli
9	907	100.0	172	5	US-10-991-653-3	Sequence 3, Appli
10	907	100.0	172	6	US-11-078-608-3	Sequence 3, Appli
11	907	100.0	172	6	US-11-040-706-3	Sequence 3, Appli

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OM protein - protein search, using sw model

Run on: April 4, 2006, 18:29:20 ; Search time 15.5 Seconds
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337.807 Million cell updates/sec

Title: US-10-825-068-3
Perfect score: 907
Sequence: 1 CYLSERLMLDARENLKLLDR.....TVSTTLQKRLTKMGDDLNSP 172

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 180808 seqs, 30441898 residues

Total number of hits satisfying chosen parameters: 180808

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA_New:*

- 1: /SIDS5/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
- 2: /SIDS5/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
- 3: /SIDS5/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
- 4: /SIDS5/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
- 5: /SIDS5/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
- 6: /SIDS5/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
- 7: /SIDS5/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
- 8: /SIDS5/ptodata/2/pubpaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	907	100.0	172	7	US-11-177-010-4	Sequence 4, Appli
2	907	100.0	172	7	US-11-112-369-2	Sequence 2, Appli
3	899	99.1	172	7	US-11-177-010-2	Sequence 2, Appli
4	899	99.1	172	7	US-11-112-369-1	Sequence 1, Appli
5	474	52.3	172	6	US-10-519-390-11	Sequence 11, Appl
6	474	52.3	194	6	US-10-936-447-20	Sequence 20, Appl
7	474	52.3	757	6	US-10-936-447-8	Sequence 8, Appli
8	441	48.6	166	7	US-11-132-722-49	Sequence 49, Appl
9	441	48.6	166	7	US-11-176-830-187	Sequence 187, App

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OM protein - protein search, using sw model

Run on: April 4, 2006, 18:22:20 ; Search time 24.5 Seconds
 (without alignments)
 675.481 Million cell updates/sec

Title: US-10-825-068-3
 Perfect score: 907
 Sequence: 1 CYLSERLMLDARENLKLLDR.....TVSTTLQKRLTKMGDDLNSP 172

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : PIR_80:*
 1: pirl:*
 2: pir2:*
 3: pir3:*
 4: pir4:*

Pred. No. is the number of results predicted by chance to have a
 score greater than or equal to the score of the result being printed,
 and is derived by analysis of the total score distribution.

SUMMARIES

Result		%					
No.	Score	Query Match	Length	DB	ID	Description	
1	901	99.3	195	2	JS0204	trophoblast interf	
2	878	96.8	195	2	I47068	trophoblast protei	
3	872	96.1	195	2	I47066	trophoblast protei	
4	869	95.8	195	2	I47069	trophoblast protei	
5	844	93.1	195	2	I46272	trophoblast interf	
6	839	92.5	172	2	A61578	trophoblast protei	
7	834	92.0	195	2	A61455	trophoblast protei	
8	810	89.3	195	2	I47067	trophoblast protei	
9	782	86.2	195	2	I47097	trophoblast protei	
10	749	82.6	184	2	I47098	trophoblast protei	
11	729	80.4	195	2	A39505	trophoblast interf	
12	727	80.2	195	2	S23751	trophoblast interf	
13	724	79.8	195	2	B39505	trophoblast protei	

OM protein - protein search, using sw model

Run on: April 4, 2006, 18:17:34 ; Search time 145.5 Seconds
 (without alignments)
 834.027 Million cell updates/sec

Title: US-10-825-068-3
 Perfect score: 907
 Sequence: 1 CYLSERLMLDARENLKLLDR.....TVSTTLQKRLTKMGDDLNSP 172

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : UniProt_05.80:*
 1: uniprot_sprot:*
 2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result		%					
No.	Score	Query Match	Length	DB	ID	Description	
1	904	99.7	195	1	IFNT2_SHEEP	P56829 ovis aries	
2	899	99.1	195	1	IFNT1_SHEEP	P56828 ovis aries	
3	896	98.8	172	1	IFNT3_SHEEP	P56832 ovis aries	
4	885	97.6	195	1	IFNT4_SHEEP	Q28594 ovis aries	
5	881	97.1	195	1	IFNT5_SHEEP	Q28595 ovis aries	
6	878	96.8	195	1	IFNT7_SHEEP	Q08071 ovis aries	
7	872	96.1	195	1	IFNT9_SHEEP	Q08070 ovis aries	
8	869	95.8	195	1	IFNT8_SHEEP	Q08072 ovis aries	
9	844	93.1	195	1	IFNT_CAPHI	P28171 capra hircu	
10	834	92.0	195	1	IFNT6_SHEEP	Q29429 ovis aries	
11	828	91.3	195	2	Q6UZ49_CAPHI	Q6uz49 capra hircu	
12	828	91.3	195	2	Q6UZ50_CAPHI	Q6uz50 capra hircu	
13	820	90.4	172	2	Q6RFZ8_SHEEP	Q6rfz8 ovis aries	
14	810	89.3	195	1	IFNTA_SHEEP	Q08053 ovis aries	
15	802	88.4	195	2	Q6UZ47_CAPHI	Q6uz47 capra hircu	

Sequence Comparison 1

RESULT 3

AAW31698

ID AAW31698 standard; protein; 172 AA.

XX

AC AAW31698;

XX

DT 14-APR-1998 (first entry)

XX

DE Mature ovine interferon-tau (OvIFNtau) protein.

XX

KW Interferon-tau; ovine; human; auto immune disease; treatment; toxicity;
KW IFN tau; multiple sclerosis; diabetes mellitus; asthma; allergy; cancer.

XX

OS Ovis aries.

XX

PN WO9733607-A1.

XX

PD 18-SEP-1997.

XX

PF 12-MAR-1997; 97WO-US003794.

XX

PR 15-MAR-1996; 96US-00616904.

XX

PA (UYFL) UNIV FLORIDA.

XX

PI Soos JM, Schiffenbauer J, Johnson HM;

XX

DR WPI; 1997-470642/43.

DR N-PSDB; AAV02288.

XX

PT Oral administration of interferon-tau for treatment of auto-immune
PT disease - avoids toxicity of interferon alpha and generates fewer
PT specific antibodies than injection.

XX

PS Claim 5; Page 31; 48pp; English.

XX

CC This is a mature ovine interferon-tau (OvIFNtau) protein. The ovine and
CC the human interferon-tau (IFN tau) can be used in the treatment of
CC mammalian diseases responsive to IFN tau. The new feature in the
CC treatment is that IFN tau is administered orally. The method is used to
CC treat immune, particularly autoimmune disease, specifically multiple
CC sclerosis (a preferred application, reducing both severity and frequency
CC of relapses), type I diabetes mellitus, lupus erythematosus, amyotrophic
CC lateral sclerosis, Crohn's disease, rheumatoid arthritis, stomatitis,
CC asthma, allergies and psoriasis, particularly in humans or dogs. IFN tau
CC is also useful for treating cancer (e.g. hairy cell leukaemia, Kaposi's
CC sarcoma and multiple myeloma), cell proliferation and viral diseases
CC (hepatitis, human immunodeficiency virus etc., including prevention of
CC maternal transmission). It is also used for increasing fertility in
CC female mammals (increasing life time of the corpus luteum). Oral
CC administration is as effective as injection but is more convenient and
CC generates a lower level of anti-IFN tau antibodies. Use of IFN tau avoids
CC the toxicity associated with use of IFN alpha

XX

SQ Sequence 172 AA;

Query Match

100.0%; Score 907; DB 2; Length 172;

Best Local Similarity 100.0%; Pred. No. 1.2e-92;
Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy      1 CYLSRKMLDARENLKLLDRMNRLSPHSCLQDRKDFGLPQEMVEGDQLQKDQAFPVLYEM 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 CYLSRKMLDARENLKLLDRMNRLSPHSCLQDRKDFGLPQEMVEGDQLQKDQAFPVLYEM 60

Qy     61 LQQSFNLFYTEHSSAAWDTTLLEQLCTGLQQQLDHLDTCRGQVMGEEDSELGNMDPIVTV 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 LQQSFNLFYTEHSSAAWDTTLLEQLCTGLQQQLDHLDTCRGQVMGEEDSELGNMDPIVTV 120

Qy    121 KKYFQGIYDYLQEKGYSDCAWEIVRVEMMRALTVSTTLQKRLTKMGDDLNSP 172
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 KKYFQGIYDYLQEKGYSDCAWEIVRVEMMRALTVSTTLQKRLTKMGDDLNSP 172
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